

# SCORE Search Results Details for Application 10516759 and Search Result 20081112\_112524\_us-10-516-759-14\_copy\_24\_81.rag.

|                            |                                      |                              |                       |                             |
|----------------------------|--------------------------------------|------------------------------|-----------------------|-----------------------------|
| <a href="#">Score Home</a> | <a href="#">Retrieve Application</a> | <a href="#">SCORE System</a> | <a href="#">SCORE</a> | <a href="#">Comments /</a>  |
| <a href="#">Page</a>       | <a href="#">List</a>                 | <a href="#">Overview</a>     | <a href="#">FAQ</a>   | <a href="#">Suggestions</a> |

This page gives you Search Results detail for the Application 10516759 and Search Result 20081112\_112524\_us-10-516-759-14\_copy\_24\_81.rag.

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GenCore version 6.3  
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OM protein - protein search, using sw model

Run on: November 12, 2008, 12:08:42 ; Search time 117 Seconds  
(without alignments)  
372.434 Million cell updates/sec

Title: US-10-516-759-14\_COPY\_24\_81  
Perfect score: 350  
Sequence: 1 DIKHNRPRRDCVAEGKVCDP.....RNYSRGGVCVTHCNFLNGEP 58

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 4151667 seqs, 751288301 residues

Total number of hits satisfying chosen parameters: 4151667

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_200808:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000:\*  
4: geneseqp2001:\*  
5: geneseqp2002:\*  
6: geneseqp2003a:\*  
7: geneseqp2003b:\*

8: geneseqp2004a:\*  
 9: geneseqp2004b:\*  
 10: geneseqp2005:\*  
 11: geneseqp2006:\*  
 12: geneseqp2007:\*  
 13: geneseqp2008:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result<br>No. | Score | Query |        | DB | ID        | Description        |
|---------------|-------|-------|--------|----|-----------|--------------------|
|               |       | Match | Length |    |           |                    |
| 1             | 350   | 100.0 | 82     | 7  | ADE36725  | Ade36725 Human Erb |
| 2             | 350   | 100.0 | 89     | 7  | ADE36731  | Ade36731 Human Erb |
| 3             | 350   | 100.0 | 531    | 12 | AJE77228  | Aje77228 Human Erb |
| 4             | 350   | 100.0 | 569    | 10 | AOJ20844  | Aoj20844 Human Erb |
| 5             | 350   | 100.0 | 570    | 11 | AEH24404  | Aeh24404 HUMEGFRBB |
| 6             | 350   | 100.0 | 621    | 13 | AOG42613  | Aog42613 Human HER |
| 7             | 350   | 100.0 | 621    | 13 | AOG42228  | Aog42228 Human HER |
| 8             | 350   | 100.0 | 624    | 11 | AEH24397  | Aeh24397 HUMEGFRBB |
| 9             | 350   | 100.0 | 624    | 11 | AEH24406  | Aeh24406 HUMEGFRBB |
| 10            | 350   | 100.0 | 640    | 7  | ADE36713  | Ade36713 Human Erb |
| 11            | 350   | 100.0 | 640    | 8  | ADW39268  | Adw39268 Human Erb |
| 12            | 350   | 100.0 | 699    | 11 | AEH24399  | Aeh24399 HUMEGFRBB |
| 13            | 350   | 100.0 | 857    | 13 | AOG42248  | Aog42248 Human HER |
| 14            | 350   | 100.0 | 866    | 13 | AOG42602  | Aog42602 Human HER |
| 15            | 350   | 100.0 | 1298   | 11 | AEK41239  | Aek41239 Human tyr |
| 16            | 350   | 100.0 | 1300   | 10 | AOJ20843  | Aoj20843 Human Erb |
| 17            | 350   | 100.0 | 1302   | 10 | AOJ20845  | Aoj20845 Human Erb |
| 18            | 350   | 100.0 | 1342   | 2  | AAR13833  | Aar13833 HER-3 epi |
| 19            | 350   | 100.0 | 1342   | 2  | AAR88453  | Aar88453 erbB-3 po |
| 20            | 350   | 100.0 | 1342   | 2  | AAW69406  | Aaw69406 ErbB-3 gl |
| 21            | 350   | 100.0 | 1342   | 2  | AAAY16594 | Aay16594 erbB-3 pr |
| 22            | 350   | 100.0 | 1342   | 4  | AAG65359  | Aag65359 Human Her |
| 23            | 350   | 100.0 | 1342   | 6  | ADE62708  | Ade62708 Human Pro |
| 24            | 350   | 100.0 | 1342   | 6  | ADB67646  | Adb67646 Human epi |
| 25            | 350   | 100.0 | 1342   | 6  | ADB67617  | Adb67617 Human epi |
| 26            | 350   | 100.0 | 1342   | 6  | ADB67645  | Adb67645 Human epi |
| 27            | 350   | 100.0 | 1342   | 6  | ADB67647  | Adb67647 Human epi |
| 28            | 350   | 100.0 | 1342   | 6  | ADB67642  | Adb67642 Human epi |
| 29            | 350   | 100.0 | 1342   | 6  | ADB67644  | Adb67644 Human epi |
| 30            | 350   | 100.0 | 1342   | 6  | ADB67643  | Adb67643 Human epi |
| 31            | 350   | 100.0 | 1342   | 6  | ADN39920  | Adn39920 Cancer/an |
| 32            | 350   | 100.0 | 1342   | 7  | ADA37256  | Ada37256 Human Erb |
| 33            | 350   | 100.0 | 1342   | 7  | ADM10301  | Adm10301 Human epi |

|    |     |       |      |    |          |          |           |      |
|----|-----|-------|------|----|----------|----------|-----------|------|
| 34 | 350 | 100.0 | 1342 | 7  | ADD52685 | Add52685 | Human     | erb  |
| 35 | 350 | 100.0 | 1342 | 7  | ADE36712 | Ade36712 | Human     | Erb  |
| 36 | 350 | 100.0 | 1342 | 8  | ADW39267 | Adw39267 | Human     | Erb  |
| 37 | 350 | 100.0 | 1342 | 8  | ADJ66656 | Adj66656 | Her3      | prot |
| 38 | 350 | 100.0 | 1342 | 8  | ADO56208 | Ado56208 | Human     | Erb  |
| 39 | 350 | 100.0 | 1342 | 8  | ADP54346 | Adp54346 | Human     | PRO  |
| 40 | 350 | 100.0 | 1342 | 8  | ADQ19366 | Adq19366 | Human     | sof  |
| 41 | 350 | 100.0 | 1342 | 9  | AJU90553 | Aju90553 | Human     | ERB  |
| 42 | 350 | 100.0 | 1342 | 10 | ADX05662 | Adx05662 | Cyclin-de |      |
| 43 | 350 | 100.0 | 1342 | 10 | ADZ72376 | Adz72376 | Human     | epi  |
| 44 | 350 | 100.0 | 1342 | 10 | AEB87743 | Aeb87743 | Human     | ERB  |
| 45 | 350 | 100.0 | 1342 | 10 | AEC21999 | Aec21999 | Human     | ERB  |

## ALIGNMENTS

## RESULT 1

## ADE36725

ID ADE36725 standard; protein; 82 AA.

XX

AC ADE36725;

XX

DT 29-JAN-2004 (first entry)

XX

DE Human ErbB-3-fl2 amino acid sequence SEQ ID NO:14.

XX

KW neoplasm; ErbB-3; immune response; cytostatic; gene therapy; cancer;  
KW human.

XX

OS Homo sapiens.

XX

PN WO2003080835-A1.

XX

PD 02-OCT-2003.

XX

PF 26-MAR-2003; 2003WO-CN000217.

XX

PR 26-MAR-2002; 2002CN-00116259.

XX

PA (ZENS-) ZENSUN SHANGHAI SCI TECH LTD.

XX

PI Zhou M;

XX

DR WPI; 2003-876924/81.

XX

PT Use of an ErbB-3 protein, a nucleic acid encoding an ErbB-3 protein or  
PT their fragments, for treating, preventing or delaying neoplasms (e.g.  
PT urethra, uterus, vagina or vulva neoplasm) or cancers (e.g. breast, ovary



OS Homo sapiens.  
XX  
PN WO2003080835-A1.  
XX  
PD 02-OCT-2003.  
XX  
PF 26-MAR-2003; 2003WO-CN000217.  
XX  
PR 26-MAR-2002; 2002CN-00116259.  
XX  
PA (ZENS-) ZENSUN SHANGHAI SCI TECH LTD.  
XX  
PI Zhou M;  
XX  
DR WPI; 2003-876924/81.  
DR N-PSDB; ADE36730.  
XX  
PT Use of an ErbB-3 protein, a nucleic acid encoding an ErbB-3 protein or  
PT their fragments, for treating, preventing or delaying neoplasms (e.g.  
PT urethra, uterus, vagina or vulva neoplasm) or cancers (e.g. breast, ovary  
PT or colon cancer).  
XX  
PS Claim 22; Fig 23; 68pp; English.  
XX  
CC The present invention describes a method for treating, preventing or  
CC delaying neoplasm in a mammal. The method comprises administering an ErbB  
CC -3 protein, a nucleic acid encoding an ErbB-3 protein, or their  
CC functional fragments, where an immune response is generated against the  
CC neoplasm. ErbB-3 has cytostatic activity, and can be used in gene  
CC therapy. The method is useful for treating, preventing or delaying  
CC neoplasms (e.g. adrenal gland, anus, auditory nerve, bile ducts, bladder,  
CC bone, brain, breast, buccal, central nervous system, cervix, colon, ear,  
CC endometrium, oesophagus, eye, eyelids, fallopian tube, gastrointestinal  
CC tract, head and neck, heart, kidney, larynx, liver, lung, mandible,  
CC mandibular condyle, maxilla, mouth, nasopharynx, nose, oral cavity,  
CC ovary, pancreas, parotid gland, penis, pinna, pituitary, prostate gland,  
CC rectum, retina, salivary glands, skin, small intestine, spinal cord,  
CC stomach, testes, thyroid, tonsil, urethra, uterus, vagina,  
CC vestibulocochlear nerve, or vulva neoplasm), or cancers (breast, ovary,  
CC stomach, prostate, colon and lung cancer). The present sequence  
CC represents a human ErbB-3 amino acid sequence, which is used in the  
CC exemplification of the present invention. N.B. The present sequence is  
CC designated as SEQ ID NO:14 in figure 23 but does not correspond with the  
CC SEQ ID NO:14 given in the Sequence Listing.  
XX  
SQ Sequence 89 AA;

Query Match 100.0%; Score 350; DB 7; Length 89;  
Best Local Similarity 100.0%; Pred. No. 7e-28;

Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 DIKHNRPRRDCVAEGKVC DPLCSSGGCWGPGPGQCLSCRNYSRGGVCVTHCNFLNGEP 58
      |||||||||||||||||||
Db      24 DIKHNRPRRDCVAEGKVC DPLCSSGGCWGPGPGQCLSCRNYSRGGVCVTHCNFLNGEP 81
```

## RESULT 3

AJE77228

ID AJE77228 standard; protein; 531 AA.

XX

AC AJE77228;

XX

DT 18-OCT-2007 (first entry)

XX

DE Human ErbB3 tyrosine kinase receptor ectodomain protein (aa: 1-531).

XX

KW Diagnosis; prognosis; therapeutic; cancer;

KW ErbB3 tyrosine kinase receptor.

XX

OS Homo sapiens.

XX

PN WO2007092932-A2.

XX

PD 16-AUG-2007.

XX

PF 08-FEB-2007; 2007WO-US061863.

XX

PR 08-FEB-2006; 2006US-0771237P.

PR 05-OCT-2006; 2006US-0828343P.

XX

PA (TARG-) TARGETED MOLECULAR DIAGNOSTICS LLC.

PA (YEDA ) YEDA RES &amp; DEV CO LTD.

XX

PI Bacus SS, Hill JE, Yarden Y, Kochupurakkal BS;

XX

DR WPI; 2007-690352/64.

DR N-PSDB; AJE77227.

DR REFSEQ; NP\_001973.

XX

PT New bivalent binding molecule having binding affinity for ErbB ligand at  
PT separate binding sites in a single covalently joined protein molecule,  
PT useful for treating a disease or condition by removal or inhibition of an  
PT ErbB ligand.

XX

PS Claim 10; SEQ ID NO 6; 37pp; English.

XX

CC The present invention relates to new bivalent ErbB-based ligand binding  
CC molecules along with their method of preparation and use. The binding

SQ Sequence 531 AA;

```
Query Match      100.0%;  Score 350;  DB 12;  Length 531;
Best Local Similarity 100.0%;  Pred. No. 3.6e-27;
Matches    58;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

Qy 1 DIKHNRRPRDCVAEGKVC DPLCSSGGCWGPGPGQCLSCRNYSRGGVCVTHCNFLNGEP 58  
 ||||||||||||||||||  
 Db 464 DIKHNRRPRDCVAEGKVC DPLCSSGGCWGPGPGQCLSCRNYSRGGVCVTHCNFLNGEP 521

AOJ20844

ID A0J20844 standard; protein; 569 AA.

AC A0J20844;

DT 06-MAR-2008 (first entry)

DE Human ErbB3 receptor tyrosine kinase protein SEQ:97.

KW splicing; gene identification signature analysis; therapeutic; diagnosis;  
KW cancer; cytostatic; inflammation; antiinflammatory; autoimmune disease;  
KW immunosuppressive; graft rejection.

OS Homo sapiens.

PN WO2005071059-A2.

PD 04-AUG-2005.

PF 27-JAN-2005; 2005WO-IL000107.

PR 27-JAN-2004; 2004US-0539128P.

PR 15-JUN-2004; 2004US-0579202P.

PA (COMP-) COMPUGEN LTD.

XX

PI Sorek R, Pollock S, Diber A, Levine Z, Nemzer S, Kol G, Wool A;  
PI Haviv A, Cohen Y, Cohen Y, Shemesh R, Savitsky K;

XX

DR WPI; 2005-555488/56.

XX

PT Identifying alternatively spliced exons, involves scoring each of several  
PT exon sequences derived from genes of species according to one or more  
PT sequence parameters.

XX

PS Example 3; SEQ ID NO 97; 991pp; English.

XX

The present invention relates to a novel method of identifying (M1) alternatively spliced exons. The method comprises scoring each of several exon sequences derived from genes of a species according to at least one sequence parameter, where the exon sequences of the several exon sequences scoring above a predetermined threshold represent alternatively spliced exons, thus identifying the alternatively spliced exons. Also claimed are: a system (S1) for generating a database of alternatively spliced exons; predicting (M2) expression products of a gene of interest and analyzing chromosomal location of each of the alternatively spliced exons with respect to coding sequence of the gene of interest to thus predict expression products of the gene of interest. (M1) is useful for identifying alternatively spliced exons. (S1) is useful for generating a database of alternatively spliced exons. The DNA and the protein sequences of the invention are useful for the diagnosis and/or treatment of the diseases like cancer, inflammatory disease, autoimmune disease, allergy and graft rejection. The present sequence represents a human ErbB3 receptor tyrosine kinase protein.

XX

SQ Sequence 569 AA;

Query Match 100.0%; Score 350; DB 10; Length 569;  
Best Local Similarity 100.0%; Pred. No. 3.8e-27;  
Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIKHNRPRRDCVAEGKVC DPLCSSGGCWGPGPGQCLSCRNYSRGGVCVTHCNFLNGEP 58  
 |||  
 Db 483 DIKHNRPRRDCVAEGKVC DPLCSSGGCWGPGPGQCLSCRNYSRGGVCVTHCNFLNGEP 540

## RESULT 5

AEH24404

ID AEH24404 standard; protein; 570 AA.

XX

AC AEH24404;

XX



DT 29-JUN-2006 (first entry)  
 XX  
 DE HUMEGRFRBB3\_PEA\_1\_P53 polypeptide.  
 XX  
 KW diagnostic; prognosis; genetic marker; screening; cancer; cytostatic;  
 KW neoplasm; HUMEGRFRBB3\_PEA\_1\_P53; protein-tyrosine kinase erbB-3 precursor;  
 KW ERBB3.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2006043271-A1.  
 XX  
 PD 27-APR-2006.  
 XX  
 PF 16-OCT-2005; 2005WO-IL001096.  
 XX  
 PR 22-OCT-2004; 2004US-0621004P.  
 PR 18-NOV-2004; 2004US-0628529P.  
 XX  
 PA (COMP-) COMPUGEN LTD.  
 XX  
 PI Novik A, Pollock S, Levine Z, Dahary D, Sorek R, Sella-Tavor O;  
 PI Cohen-Dayag A, Sameach-Greenwald S, Walach S;  
 XX  
 DR WPI; 2006-331789/34.  
 DR N-PSDB; AEH24321.  
 XX  
 PT New isolated polynucleotide and polypeptide markers, useful as diagnostic  
 PT markers for diagnosing diseases, predicting response to treatment,  
 PT monitoring treatment, or determining prognosis of a marker-detectable  
 PT disease.  
 XX  
 PS Example 5; SEQ ID NO 144; 421pp; English.  
 XX  
 CC The invention describes an isolated polynucleotide comprising  
 CC HUMA1ACM\_PEA 2 \_T21, HUMA1ACM\_PEA 2 \_T27, or HUMA1ACM\_PEA 2 \_T7  
 CC comprising 1320, 1239, or 2713 bp (SEQ ID NO. 1, 2, or 3). Also described  
 CC are: an isolated polypeptide selected from HUMA1ACM\_PEA 2 \_P36 (SEQ ID  
 CC NO. 51), HUMA1ACM\_PEA 2 \_P49 (SEQ ID NO. 52), or HUMA1ACM\_PEA 2 \_P59 (SEQ  
 CC ID NO. 53); an isolated polypeptide encoding for a head of: (a)  
 CC HUMA1ACM\_PEA 2 \_P36 comprising a polypeptide 70% homologous to SEQ ID NO.  
 CC 180 or 182 of HUMA1ACM\_PEA 2 \_P36; (b) HUMA1ACM\_PEA 2 \_P49 comprising a  
 CC polypeptide 70% homologous to SEQ ID NO. 182 of HUMA1ACM\_PEA 2 \_P49; or  
 CC (c) HUMA1ACM\_PEA 2 \_P59 comprising a polypeptide 70% homologous to SEQ ID  
 CC NO. 182 of HUMA1ACM\_PEA 2 \_P59; an isolated polypeptide encoding for a  
 CC tail of: (a) HUMA1ACM\_PEA 2 \_P36 comprising a polypeptide 70% homologous  
 CC to SEQ ID NO. 181 in HUMA1ACM\_PEA 2 \_P36; (b) HUMA1ACM\_PEA 2 \_P49  
 CC comprising a polypeptide 70% homologous to SEQ ID NO. 183 in HUMA1ACM\_PEA  
 CC 2 \_P49; or (c) HUMA1ACM\_PEA 2 \_P59 comprising a polypeptide 70%

homologous to SEQ ID NO. 185 or 208 in HUMA1ACM\_PEA 2 \_P59; a primer pair comprising a pair of isolated oligonucleotides capable of amplifying the amplicon; an antibody capable of specifically binding to an epitope of the amino acid sequence; a kit for detecting a marker-detectable disease comprising a kit detecting specific expression of a splice variant; a biomarker capable of detecting marker-detectable disease comprising the nucleic acid sequences or amino acid sequence, or its fragments. The polynucleotides and polypeptides are useful as diagnostic markers for diagnosing and screening for diseases e.g., cancer, selecting a therapy for a marker-detectable disease and determining prognosis of a marker-detectable disease, as well as for predicting response to treatment and monitoring treatment. This sequence represents a HUMEGFRBB3\_PEA\_1\_P53 polypeptide, a transcript from the HUMEGFRBB3 cluster and variant of protein-tyrosine kinase erbB-3 precursor useful as a diagnostic marker.

XX

SQ Sequence 570 AA;

|                       |         |                    |        |                                 |
|-----------------------|---------|--------------------|--------|---------------------------------|
| Query Match           | 100.0%; | Score 350;         | DB 11; | Length 570;                     |
| Best Local Similarity | 100.0%; | Pred. No. 3.8e-27; |        |                                 |
| Matches               | 58;     | Conservative       | 0;     | Mismatches 0; Indels 0; Gaps 0; |

Qy            1 DIKHNRPRRDCVAEGKVC DPLCSSGGCWGP GPGQCLSCRNYSRGGVCVTHCNFLNGEP    58  
             |||||  
Db           483 DIKHNRPRRDCVAEGKVC DPLCSSGGCWGP GPGQCLSCRNYSRGGVCVTHCNFLNGEP    540

## RESULT 6

AOG42613

ID AOG42613 standard; protein; 621 AA.

XX

AC AOG42613;

XX

DT 06-MAR-2008 (first entry)

XX

DE Human HER3 receptor extracellular domain (HF310) mutant protein.

XX

KW Therapeutic; cancer; cytostatic; pancreas tumor; stomach tumor;  
KW head & neck tumor; uterine cervix tumor; lung tumor; colorectal tumor;  
KW endometroid carcinoma; prostate tumor; esophagus tumor; ovary tumor;  
KW uterus tumor; glioma; bladder tumor; renal tumor; breast tumor;  
KW hyperproliferation; ocular disease; ophthalmological;  
KW diabetic retinopathy; antidiabetic; psoriasis; antipsoriatic; restenosis;  
KW vasotropic; stenosis; atherosclerosis; antiarteriosclerotic;  
KW chronic obstructive airway disease; respiratory-gen.; inflammation;  
KW antiinflammatory; angiogenesis disorder; antiangiogenic; gene therapy;  
KW HER3; receptor; ErbB3; mutein.

XX

OS Homo sapiens.

OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 541  
FT /note= "Wild type Gly replaced with Glu"  
XX  
PN WO2007146959-A2.  
XX  
PD 21-DEC-2007.  
XX  
PF 12-JUN-2007; 2007WO-US071041.  
XX  
PR 12-JUN-2006; 2006US-0813260P.  
PR 29-SEP-2006; 2006US-0848542P.  
PR 05-JAN-2007; 2007US-0878941P.  
XX  
PA (RECE-) RECEPTOR BIOLOGIX INC.  
XX  
PI Shepard HM, Jin P, Burton LE, Beryt M;  
XX  
DR WPI; 2008-B51284/10.  
XX  
PT New multimer comprising extracellular domain ECD from HER1 receptor,  
PT useful for treating cancer, inflammatory disease, angiogenic disease or  
PT hyperproliferative disease.  
XX  
PS Disclosure; Page; 320pp; English.  
XX  
CC The present invention provides pan-cell surface receptor specific  
CC therapeutics including and pan-HER (also referred to as ErbB or EGFR)  
CC specific therapeutics that interact with at least two different HER  
CC receptor ligands and/or dimerize with or interact with two or more HER  
CC cell surface receptors. The invention is useful for treating cancer such  
CC as pancreatic, gastric, head and neck, cervical, lung, colorectal,  
CC endometrial, prostate, esophageal, ovarian, uterine, glioma, bladder,  
CC renal and breast cancer, proliferative diseases such as proliferation  
CC and/or migration of smooth muscle cells, disease of the anterior eye,  
CC diabetic retinopathy, psoriasis, restenosis, ophthalmic disorders,  
CC stenosis, atherosclerosis, hypertension from thickening of blood vessels,  
CC bladder diseases and obstructive airway diseases, inflammatory disease  
CC and angiogenic disease. The invention is also useful in gene therapy. The  
CC present sequence is human HER3 receptor (ErbB3) extracellular domain  
CC mutant protein. Note: This sequence is not shown in the specification,  
CC but is derived from human HER3 receptor ECD protein shown as SEQ ID NO:  
CC 26 in sequence listing of the specification.  
XX  
SQ Sequence 621 AA;

Query Match 100.0%; Score 350; DB 13; Length 621;

Best Local Similarity 100.0%; Pred. No. 4.1e-27;

Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIKHNRPRRDCVAEGKVC DPLCSSGGCWGPGPGQCLSCRNYSRGGVCVTHCNFLNGEP 58  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 464 DIKHNRPRRDCVAEGKVC DPLCSSGGCWGPGPGQCLSCRNYSRGGVCVTHCNFLNGEP 521

## RESULT 7

AOG42228

ID AOG42228 standard; protein; 621 AA.

XX

AC AOG42228;

XX

DT 06-MAR-2008 (first entry)

XX

DE Human HER3 receptor extracellular domain protein, HF310.

XX

KW Therapeutic; cancer; cytostatic; pancreas tumor; stomach tumor;

KW head &amp; neck tumor; uterine cervix tumor; lung tumor; colorectal tumor;

KW endometroid carcinoma; prostate tumor; esophagus tumor; ovary tumor;

KW uterus tumor; glioma; bladder tumor; renal tumor; breast tumor;

KW hyperproliferation; ocular disease; ophthalmological;

KW diabetic retinopathy; antidiabetic; psoriasis; antipsoriatic; restenosis;

KW vasotropic; stenosis; atherosclerosis; antiarteriosclerotic;

KW chronic obstructive airway disease; respiratory-gen.; inflammation;

KW antiinflammatory; angiogenesis disorder; antiangiogenic; gene therapy;

KW HER3; receptor; ErbB3.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Misc-difference 541

FT /note= "Encoded by GAG"

XX

PN WO2007146959-A2.

XX

PD 21-DEC-2007.

XX

PF 12-JUN-2007; 2007WO-US071041.

XX

PR 12-JUN-2006; 2006US-0813260P.

PR 29-SEP-2006; 2006US-0848542P.

PR 05-JAN-2007; 2007US-0878941P.

XX

PA (RECE-) RECEPTOR BIOLOGIX INC.

XX

PI Shepard HM, Jin P, Burton LE, Beryt M;

XX

Qy 1 DIKHNRPRRDCVAEGKVC DPLCSSGGCWGPGPGQCLSCRNYSRGGVCVTHCNFLNGEP 58  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 464 DIKHNRPRRDCVAEGKVC DPLCSSGGCWGPGPGQCLSCRNYSRGGVCVTHCNFLNGEP 521

http://es/ScoreAccessWeb/GetItem.action?AppId=10516...10-516-759-14\_copy\_24\_81.rag&ItemType=4&startByte=0 (13 of 26)11/22/2008 11:34:49 AM

XX  
OS Homo sapiens.  
XX  
PN WO2006043271-A1.  
XX  
PD 27-APR-2006.  
XX  
PF 16-OCT-2005; 2005WO-IL001096.  
XX  
PR 22-OCT-2004; 2004US-0621004P.  
PR 18-NOV-2004; 2004US-0628529P.  
XX  
PA (COMP-) COMPUGEN LTD.  
XX  
PI Novik A, Pollock S, Levine Z, Dahary D, Sorek R, Sella-Tavor O;  
PI Cohen-Dayag A, Sameach-Greenwald S, Walach S;  
XX  
DR WPI; 2006-331789/34.  
DR N-PSDB; AEH24320.  
XX  
PT New isolated polynucleotide and polypeptide markers, useful as diagnostic  
PT markers for diagnosing diseases, predicting response to treatment,  
PT monitoring treatment, or determining prognosis of a marker-detectable  
PT disease.  
XX  
PS Example 5; SEQ ID NO 137; 421pp; English.  
XX  
CC The invention describes an isolated polynucleotide comprising  
CC HUMA1ACM\_PEA 2 \_T21, HUMA1ACM\_PEA 2 \_T27, or HUMA1ACM\_PEA 2 \_T7  
CC comprising 1320, 1239, or 2713 bp (SEQ ID NO. 1, 2, or 3). Also described  
CC are: an isolated polypeptide selected from HUMA1ACM\_PEA 2 \_P36 (SEQ ID  
CC NO. 51), HUMA1ACM\_PEA 2 \_P49 (SEQ ID NO. 52), or HUMA1ACM\_PEA 2 \_P59 (SEQ  
CC ID NO. 53); an isolated polypeptide encoding for a head of: (a)  
CC HUMA1ACM\_PEA 2 \_P36 comprising a polypeptide 70% homologous to SEQ ID NO.  
CC 180 or 182 of HUMA1ACM\_PEA 2 \_P36; (b) HUMA1ACM\_PEA 2 \_P49 comprising a  
CC polypeptide 70% homologous to SEQ ID NO. 182 of HUMA1ACM\_PEA 2 \_P49; or  
CC (c) HUMA1ACM\_PEA 2 \_P59 comprising a polypeptide 70% homologous to SEQ ID  
CC NO. 182 of HUMA1ACM\_PEA 2 \_P59; an isolated polypeptide encoding for a  
CC tail of: (a) HUMA1ACM\_PEA 2 \_P36 comprising a polypeptide 70% homologous  
CC to SEQ ID NO. 181 in HUMA1ACM\_PEA 2 \_P36; (b) HUMA1ACM\_PEA 2 \_P49  
CC comprising a polypeptide 70% homologous to SEQ ID NO. 183 in HUMA1ACM\_PEA  
CC 2 \_P49; or (c) HUMA1ACM\_PEA 2 \_P59 comprising a polypeptide 70%  
CC homologous to SEQ ID NO. 185 or 208 in HUMA1ACM\_PEA 2 \_P59; a primer pair  
CC comprising a pair of isolated oligonucleotides capable of amplifying the  
CC amplicon; an antibody capable of specifically binding to an epitope of  
CC the amino acid sequence; a kit for detecting a marker-detectable disease  
CC comprising a kit detecting specific expression of a splice variant; a  
CC biomarker capable of detecting marker-detectable disease comprising the  
CC nucleic acid sequences or amino acid sequence, or its fragments. The

polynucleotides and polypeptides are useful as diagnostic markers for diagnosing and screening for diseases e.g., cancer, selecting a therapy for a marker-detectable disease and determining prognosis of a marker-detectable disease, as well as for predicting response to treatment and monitoring treatment. This sequence represents a HUMEGFRBB3\_PEA\_1\_P15 polypeptide, a transcript from the HUMEGFRBB3 cluster and variant of protein-tyrosine kinase erbB-3 precursor useful as a diagnostic marker.

XX

SQ Sequence 624 AA;

|                       |         |                    |        |                                 |
|-----------------------|---------|--------------------|--------|---------------------------------|
| Query Match           | 100.0%; | Score 350;         | DB 11; | Length 624;                     |
| Best Local Similarity | 100.0%; | Pred. No. 4.1e-27; |        |                                 |
| Matches               | 58;     | Conservative       | 0;     | Mismatches 0; Indels 0; Gaps 0; |

Qy 1 DIKHNRRPRDCVAEGKVC DPLCSSGGCWGPGPGQCLSCRNYSRGGVCVTHCNFLNGEP 58  
 |||  
 Db 483 DIKHNRRPRDCVAEGKVC DPLCSSGGCWGPGPGQCLSCRNYSRGGVCVTHCNFLNGEP 540

## RESULT 9

AEH24406

ID AEH24406 standard; protein; 624 AA.

XX

AC AEH24406;

XX

DT 29-JUN-2006 (first entry)

XX

DE HUMEGFRBB3\_PEA\_1\_P55 polypeptide.

XX

KW diagnostic; prognosis; genetic marker; screening; cancer; cytostatic;  
KW neoplasm; HUMEGFRBB3\_PEA\_1\_P55; protein-tyrosine kinase erbB-3 precursor;  
KW ERBB3.

XX

OS Homo sapiens.

XX

PN WO2006043271-A1.

XX

PD 27-APR-2006.

XX

PF 16-OCT-2005; 2005WO-IL001096.

XX

PR 22-OCT-2004; 2004US-0621004P.

PR 18-NOV-2004; 2004US-0628529P.

XX

PA (COMP-) COMPUGEN LTD.

XX

PI Novik A, Pollock S, Levine Z, Dahary D, Sorek R, Sella-Tavor O;

PI Cohen-Dayag A, Sameach-Greenwald S, Walach S;

XX

DR WPI; 2006-331789/34.

DR N-PSDB; AEH24323.

XX

PT New isolated polynucleotide and polypeptide markers, useful as diagnostic  
PT markers for diagnosing diseases, predicting response to treatment,  
PT monitoring treatment, or determining prognosis of a marker-detectable  
PT disease.

XX

PS Example 5; SEQ ID NO 146; 421pp; English.

XX

CC The invention describes an isolated polynucleotide comprising  
CC HUMA1ACM\_PEA 2 \_T21, HUMA1ACM\_PEA 2 \_T27, or HUMA1ACM\_PEA 2 \_T7  
CC comprising 1320, 1239, or 2713 bp (SEQ ID NO. 1, 2, or 3). Also described  
CC are: an isolated polypeptide selected from HUMA1ACM\_PEA 2 \_P36 (SEQ ID  
CC NO. 51), HUMA1ACM\_PEA 2 \_P49 (SEQ ID NO. 52), or HUMA1ACM\_PEA 2 \_P59 (SEQ  
CC ID NO. 53); an isolated polypeptide encoding for a head of: (a)  
CC HUMA1ACM\_PEA 2 \_P36 comprising a polypeptide 70% homologous to SEQ ID NO.  
CC 180 or 182 of HUMA1ACM\_PEA 2 \_P36; (b) HUMA1ACM\_PEA 2 \_P49 comprising a  
CC polypeptide 70% homologous to SEQ ID NO. 182 of HUMA1ACM\_PEA 2 \_P49; or  
CC (c) HUMA1ACM\_PEA 2 \_P59 comprising a polypeptide 70% homologous to SEQ ID  
CC NO. 182 of HUMA1ACM\_PEA 2 \_P59; an isolated polypeptide encoding for a  
CC tail of: (a) HUMA1ACM\_PEA 2 \_P36 comprising a polypeptide 70% homologous  
CC to SEQ ID NO. 181 in HUMA1ACM\_PEA 2 \_P36; (b) HUMA1ACM\_PEA 2 \_P49  
CC comprising a polypeptide 70% homologous to SEQ ID NO. 183 in HUMA1ACM\_PEA  
CC 2 \_P49; or (c) HUMA1ACM\_PEA 2 \_P59 comprising a polypeptide 70%  
CC homologous to SEQ ID NO. 185 or 208 in HUMA1ACM\_PEA 2 \_P59; a primer pair  
CC comprising a pair of isolated oligonucleotides capable of amplifying the  
CC amplicon; an antibody capable of specifically binding to an epitope of  
CC the amino acid sequence; a kit for detecting a marker-detectable disease  
CC comprising a kit detecting specific expression of a splice variant; a  
CC biomarker capable of detecting marker-detectable disease comprising the  
CC nucleic acid sequences or amino acid sequence, or its fragments. The  
CC polynucleotides and polypeptides are useful as diagnostic markers for  
CC diagnosing and screening for diseases diseases e.g., cancer, selecting a  
CC therapy for a marker-detectable disease and determining prognosis of a  
CC marker-detectable disease, as well as for predicting response to  
CC treatment and monitoring treatment. This sequence represents a  
CC HUMEGFRBB3\_PEA\_1\_P55 polypeptide, a transcript from the HUMEGFRBB3  
CC cluster and variant of protein-tyrosine kinase erbB-3 precursor useful as  
CC a diagnostic marker.

XX

SQ Sequence 624 AA;

Query Match 100.0%; Score 350; DB 11; Length 624;  
Best Local Similarity 100.0%; Pred. No. 4.1e-27;  
Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy

1 DIKHNRPRRDCVAEGKVC DPLCSSGGCWGPGPGQCLSCRNYSRGGVCVTHCNFLNGEP 58



Db 483 DIKHNRPRRDCVAEGKVC DPLCSSGGCWGPGPGQCLSCRNYSRGGVCVTHCNFLNGEP 540

RESULT 10

ADE36713

ID ADE36713 standard; protein; 640 AA.  
XX  
AC ADE36713;  
XX  
DT 29-JAN-2004 (first entry)  
XX  
DE Human ErbB-3 partial amino acid sequence SEQ ID NO:2.  
XX  
KW neoplasm; ErbB-3; immune response; cytostatic; gene therapy; cancer;  
KW human.  
XX  
OS Homo sapiens.  
XX  
PN WO2003080835-A1.  
XX  
PD 02-OCT-2003.  
XX  
PF 26-MAR-2003; 2003WO-CN000217.  
XX  
PR 26-MAR-2002; 2002CN-00116259.  
XX  
PA (ZENS-) ZENSUN SHANGHAI SCI TECH LTD.  
XX  
PI Zhou M;  
XX  
DR WPI; 2003-876924/81.  
XX  
PT Use of an ErbB-3 protein, a nucleic acid encoding an ErbB-3 protein or  
PT their fragments, for treating, preventing or delaying neoplasms (e.g.  
PT urethra, uterus, vagina or vulva neoplasm) or cancers (e.g. breast, ovary  
PT or colon cancer).  
XX  
PS Claim 22; SEQ ID NO 2; 68pp; English.  
XX  
CC The present invention describes a method for treating, preventing or  
CC delaying neoplasm in a mammal. The method comprises administering an ErbB  
CC -3 protein, a nucleic acid encoding an ErbB-3 protein, or their  
CC functional fragments, where an immune response is generated against the  
CC neoplasm. ErbB-3 has cytostatic activity, and can be used in gene  
CC therapy. The method is useful for treating, preventing or delaying  
CC neoplasms (e.g. adrenal gland, anus, auditory nerve, bile ducts, bladder,  
CC bone, brain, breast, buccal, central nervous system, cervix, colon, ear,  
CC endometrium, oesophagus, eye, eyelids, fallopian tube, gastrointestinal

Qy 1 DIKHNRPRRDCVAEGKVC DPLCSSGGCWGP GPGQCLSCRNYSRGGVCVTHCNFLNGEP 58  
 |||  
 Db 483 DIKHNRPRRDCVAEGKVC DPLCSSGGCWGP GPGQCLSCRNYSRGGVCVTHCNFLNGEP 540

http://es/ScoreAccessWeb/GetItem.action?AppId=10516...10-516-759-14\_copy\_24\_81.rag&ItemType=4&startByte=0 (18 of 26)11/22/2008 11:34:49 AM



PI Cohen-Dayag A, Sameach-Greenwald S, Walach S;  
XX  
DR WPI; 2006-331789/34.  
DR N-PSDB; AEH24326.  
XX  
PT New isolated polynucleotide and polypeptide markers, useful as diagnostic  
PT markers for diagnosing diseases, predicting response to treatment,  
PT monitoring treatment, or determining prognosis of a marker-detectable  
PT disease.  
XX  
PS Example 5; SEQ ID NO 139; 421pp; English.  
XX  
CC The invention describes an isolated polynucleotide comprising  
CC HUMA1ACM\_PEA 2 \_T21, HUMA1ACM\_PEA 2 \_T27, or HUMA1ACM\_PEA 2 \_T7  
CC comprising 1320, 1239, or 2713 bp (SEQ ID NO. 1, 2, or 3). Also described  
CC are: an isolated polypeptide selected from HUMA1ACM\_PEA 2 \_P36 (SEQ ID  
CC NO. 51), HUMA1ACM\_PEA 2 \_P49 (SEQ ID NO. 52), or HUMA1ACM\_PEA 2 \_P59 (SEQ  
CC ID NO. 53); an isolated polypeptide encoding for a head of: (a)  
CC HUMA1ACM\_PEA 2 \_P36 comprising a polypeptide 70% homologous to SEQ ID NO.  
CC 180 or 182 of HUMA1ACM\_PEA 2 \_P36; (b) HUMA1ACM\_PEA 2 \_P49 comprising a  
CC polypeptide 70% homologous to SEQ ID NO. 182 of HUMA1ACM\_PEA 2 \_P49; or  
CC (c) HUMA1ACM\_PEA 2 \_P59 comprising a polypeptide 70% homologous to SEQ ID  
CC NO. 182 of HUMA1ACM\_PEA 2 \_P59; an isolated polypeptide encoding for a  
CC tail of: (a) HUMA1ACM\_PEA 2 \_P36 comprising a polypeptide 70% homologous  
CC to SEQ ID NO. 181 in HUMA1ACM\_PEA 2 \_P36; (b) HUMA1ACM\_PEA 2 \_P49  
CC comprising a polypeptide 70% homologous to SEQ ID NO. 183 in HUMA1ACM\_PEA  
CC 2 \_P49; or (c) HUMA1ACM\_PEA 2 \_P59 comprising a polypeptide 70%  
CC homologous to SEQ ID NO. 185 or 208 in HUMA1ACM\_PEA 2 \_P59; a primer pair  
CC comprising a pair of isolated oligonucleotides capable of amplifying the  
CC amplicon; an antibody capable of specifically binding to an epitope of  
CC the amino acid sequence; a kit for detecting a marker-detectable disease  
CC comprising a kit detecting specific expression of a splice variant; a  
CC biomarker capable of detecting marker-detectable disease comprising the  
CC nucleic acid sequences or amino acid sequence, or its fragments. The  
CC polynucleotides and polypeptides are useful as diagnostic markers for  
CC diagnosing and screening for diseases diseases e.g., cancer, selecting a  
CC therapy for a marker-detectable disease and determining prognosis of a  
CC marker-detectable disease, as well as for predicting response to  
CC treatment and monitoring treatment. This sequence represents a  
CC HUMEGFRBB3\_PEA\_1\_P31 polypeptide, a transcript from the HUMEGFRBB3  
CC cluster and variant of protein-tyrosine kinase erbB-3 precursor useful as  
CC a diagnostic marker.  
XX  
SQ Sequence 699 AA;

Query Match 100.0%; Score 350; DB 11; Length 699;  
Best Local Similarity 100.0%; Pred. No. 4.6e-27;  
Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;





KW endometroid carcinoma; prostate tumor; esophagus tumor; ovary tumor;  
 KW uterus tumor; glioma; bladder tumor; renal tumor; breast tumor;  
 KW hyperproliferation; ocular disease; ophthalmological;  
 KW diabetic retinopathy; antidiabetic; psoriasis; antipsoriatic; restenosis;  
 KW vasotropic; stenosis; atherosclerosis; antiarteriosclerotic;  
 KW chronic obstructive airway disease; respiratory-gen.; inflammation;  
 KW antiinflammatory; angiogenesis disorder; antiangiogenic; gene therapy;  
 KW epidermal growth factor receptor; HER3; receptor; ErbB3;  
 KW immunoglobulin G1; IgG; fusion protein.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Region 1. .500  
 FT /note= "Human EGFR ECD"  
 FT Region 624. .627  
 FT /note= "Peptide linker"  
 FT Region 628. .858  
 FT /note= "Human IgG1 Fc"  
 FT Region 859. .860  
 FT /note= "AgeI linker"  
 FT Region 861. .866  
 FT /note= "His tag"  
 XX  
 PN WO2007146959-A2.  
 XX  
 PD 21-DEC-2007.  
 XX  
 PF 12-JUN-2007; 2007WO-US071041.  
 XX  
 PR 12-JUN-2006; 2006US-0813260P.  
 PR 29-SEP-2006; 2006US-0848542P.  
 PR 05-JAN-2007; 2007US-0878941P.  
 XX  
 PA (RECE-) RECEPTOR BIOLOGIX INC.  
 XX  
 PI Shepard HM, Jin P, Burton LE, Beryt M;  
 XX  
 DR WPI; 2008-B51284/10.  
 XX  
 PT New multimer comprising extracellular domain ECD from HER1 receptor,  
 PT useful for treating cancer, inflammatory disease, angiogenic disease or  
 PT hyperproliferative disease.  
 XX  
 PS Disclosure; SEQ ID NO 407; 320pp; English.  
 XX  
 CC The present invention provides pan-cell surface receptor specific  
 CC therapeutics including and pan-HER (also referred to as ErbB or EGFR)  
 CC specific therapeutics that interact with at least two different HER





XX

PI Schiffer HH;

XX

DR WPI; 2006-659129/68.

DR N-PSDB; AEK41238.

XX

PT Evaluating ligand for receptor tyrosine kinase, by contacting cell having  
PT kinase and bioluminescent donor moiety and second protein with  
PT fluorescent acceptor moiety with test compound, determining interaction  
PT of kinase/second protein.

XX

PS Claim 51; SEQ ID NO 114; 32pp; English.

XX

CC The present sequence is that of a human receptor tyrosine kinase (RTK)  
CC signaling ligand of the current invention. RTK signaling proteins are  
CC involved in transducing the ligand-induced RTK signal from the receptor  
CC downstream into the cell. The invention relates to evaluating whether a  
CC test compound functions as a ligand for a receptor tyrosine kinase by  
CC providing a cell comprising a RTK with a Renilla luciferase  
CC bioluminescent donor moiety and a second protein comprising a fluorescent  
CC acceptor moiety, contacting the cell with a test compound and determining  
CC whether the RTK and the second protein interact in the presence of the  
CC test compound. The method involves determining whether the receptor  
CC tyrosine kinase and the second protein are within close physical distance  
CC to each other, or whether the receptor tyrosine kinase and the second  
CC protein will dissociate such that they are no longer within close  
CC physical distance to each other. The bioluminescent donor moiety on the  
CC receptor tyrosine kinase emits light at a first wavelength in the  
CC presence of the substrate, where the energy emitted from the  
CC bioluminescent donor moiety is transferred to the fluorescent acceptor  
CC moiety on the second protein when the fluorescent acceptor moiety is in  
CC close proximity to the bioluminescent donor moiety, and where the  
CC fluorescent acceptor moiety emits light at a second wavelength.  
CC Modulation of the activity of the receptor tyrosine kinase affects the  
CC protein-protein interactions between the receptor tyrosine kinase and the  
CC second protein. The fluorescent acceptor moiety is a green fluorescent  
CC protein (GFP) 2, a yellow fluorescent protein (YFP) or a CFP moiety. The  
CC determination step involves calculating the ratio of light emissions from  
CC the fluorescent acceptor moiety and the bioluminescent donor moiety. The  
CC second protein is a signaling protein that mediates receptor tyrosine  
CC kinase function or signal transduction. The method utilizes  
CC bioluminescence resonance energy transfer (BRET) technology. The receptor  
CC tyrosine kinase is a fusion protein comprising a tyrosine kinase fused to  
CC the fluorescent donor moiety. The determining step comprises determining  
CC whether the test compound is an inverse agonist or antagonist. The method  
CC is useful for evaluating whether a test compound functions as a ligand  
CC for a receptor tyrosine kinase, and for the screening of compounds which  
CC may be useful in the treatment of diseases such as cancer. Note: The  
CC sequence data for this patent did not form part of the printed

Query Match 100.0%; Score 350; DB 11; Length 1298;  
Best Local Similarity 100.0%; Pred. No. 8.1e-27;  
Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIKHNRRPRDCVAEGKVC DPLCSSGGCWGPGPGQCLSCRNYSRGGVCVTHCNFLNGEP 58  
 |||  
 Db 439 DIKHNRRPRDCVAEGKVC DPLCSSGGCWGPGPGQCLSCRNYSRGGVCVTHCNFLNGEP 496

Search completed: November 12, 2008, 12:10:46  
Job time : 124 secs

SCORE 3.0